

Human caspase-1
Human caspase-13^a
Human caspase-4
Human caspase-5
Human caspase-12
Mouse caspase-12
Mouse caspase-11
conserved amino acids^b

```

SGSEGNVKLCSLEEAQRLWKQKSAELYPIMDKSSRTRLALICNEEFDSJIPRTGAEVDI
- GSAATLKLCPHEEFLKLCKERAGELYPIKERKORTRLALICNTEFOHMPPRNGAALIDD
- ESTDALKLCPHEEFLKLCKERAELYPIKERNRTRLALICNTEFDHLPENRGADDDP
- ESTNILKLCPREEFLBLCKNHDELYPIKEREDRRRLALICNTEFDHLPARNGAHHDD
----- QYPMVEKERRCTIASNRNKEFNYNHNHNGSELDD
SEVQDTLKLCPRDQCKIKITERAKELYPVMEKEGRTLALICNKKEDYLFDRDNADTDD
-- SLNTLKLCSPEEFLTRLCKREKTQELYPIKEANORTRKALICNTEFKHLSLRYGAKEDDD
      : * * * * *

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APPROVED	BY	CRAFTSMAN
CLASS	SUBCLASS	



Human caspase-1
Human caspase-13^a
Human caspase-4
Human caspase-5
Human caspase-12
Mouse caspase-12
Mouse caspase-11
conserved amino acids^b

Human caspase-1
Human caspase-13^a
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Human caspase-1
Human caspase-13^a
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conserved amino acids^b

Human caspase-1
Human caspase-13^a
Human caspase-4
Human caspase-5
Human caspase-12
Mouse caspase-12
Mouse caspase-11
conserved amino acids^b

TCMTMLQNLGY SVDVKNLTASD MTELEAFARHP EHKTSSTFLVF MSHGIREGICG
LGMKQLLEGDGY TVEVEKLTARD MESVLWKFAARE EHKSSDSTFLVF MSHGILDGICGT
TGKMLLEGDGY SVDEENLTARD MESALRAFATRP EHKSSDSTFLVF MSHGILEGICGT
VGMKRLQGLGY TVDEKNTLARD MESVLRAFARP EHKSSDSTFLVF MSHGILEGICGT
LGMKDLLENLGY SVGKENLTAE METALROFAARP EHQSSDSTFLVF MSHGILEGICGT
LNMQLLENLGY SVVLKENLTAE METELMQFAGRP EHQSSDSTFLVF MSHGILEGICGT
IGMKLLEDIGY DVVKEELTAEG MESEMKDFALS EHQTSSTFLVF MSHGILHICGT
* * * * *
* * * * *

KHSEQVPDILQNL NALFNNLNTKNC PSLKDKPKVILII QACRGDSPGVVW FKDSVG-VSGNL
MHSEEPDVLFPY DTFERTFNRRNC LSLKDKPKVILII QACRGANGELW VSDSP-ALADS
VHDEKPPDVLVLY DTIFQIFNNRNC LSLKDKPKVILII QACRGANGELW VRDSPA-SLEVA
AHKRRKPPDVLVLY DTIFQIFNNRNC LSLKDKPKVILII QACRGANGELW VRDSPA-SLAVI
KHMDQEPDVLVLY DTIFQIFNNRNC LSLKDKPKVILII QACRGANGELW FTTDSGKASADT
KHNNKPPDVLVLY DTIFQIFNNRNC LSLKDKPKVILII QACRGANGELW VSTNKGIATADT
MHSEKTPDVLVLY DTIFQIFNNRNC LSLKDKPKVILII QACRGANGELW IRESSK-POLCR
* * * * *

SLP-TTEEFEDD AITKAHIEKDFI AFCSSTPDNVSW RHPMTGVSFIFGR LIEHMQEYACSC
FSQ-SSENLEED AVYKTHVEKDFI AFCSSTPHNVSW RDIKKSLFIFR LITCFQKYAMCC
SSQ-SSENLEED AVYKTHVEKDFI AFCSSTPHNVSW RDTSGSIFITQ LITCFQKYAMCC
SSQ-SSENLEAD SVCKIHEKDFI AFCSSTPHNVSW RDRTRGSIFITE LITCFQKYAMCC
HGRLQGNICND AVTKAHEKDFI AFKSSTPR-----
DEERYLSCKMNN SITKAHETDFI AFKSSTPHNISW KVGKTGSLFISK LIDCFKICYWY
GVD-LPRMEAD AVKLSHVEKDFI AFYSTTPPHLSY RDKTGSYFIFR LISCFRKHACSC
* * * * *

DVEEIFRKVRFS FEQBDGRAQMP TERTVLTTRCFYL FPGH
HLEEVFRKVQGS FEKENVKAQMP VERLSMTRYFYL FPGN
HLEEVFRKVQGS FETPRAKAQMP IERLSMTRYFYL FPGN
HMEIFRKVQGS FEVPAKAQMP IERATLTDRFYL FPGN
-----SHS FETPNILQPT IERLSMTRYFYL FPGN
HLEEIFRKVQGS FEVGEILTQMP IERVSMTTRYFYL FPGN
HURDIFLKVQGS FEKASIHQMP IDRATLTTRYFYL FPGN
* * * * *

FIGURE 1B

APPROVED	BY	CLASS
FIG. 1B		SUBCLASS

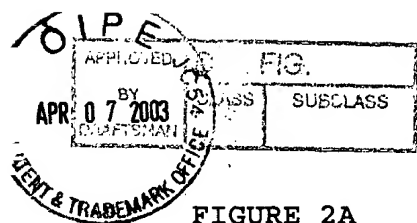


FIGURE 2A

hCaspase12

KW-Ap
KW-Bp
KW-Cp
KW-Dp
KW-Ep
KW-Fp
KW-Hp
KW-Gp
KW-Ip
KW-Jp
KW-Kp

MADEKPSNGVLVHVMVKLLIKTFLDGI FDDL MENNV LNTDEIHLIGKCLKFVVSNAENLVD
MADEKPSNGVLVHVMVKLLIKTFLDGI FDDL MENNV LNTDEIHLIGKCLKFVVSNAENLVD
MADEKPSNGVLVHVMVKLLIKTFLDGI FDDL MENNV LNTDEIHLIGKCLKFVVSNAE-LVD
MADEKPSNGVLVHVMVKLLIKTFLDGI FDDL MENNV LNTDEIHLIGKCLKFVVSNAENLVD
MADEKPSNGVLVHVMVKLLIKTFLDGI FDDL MENNV LNTDEIHLIGKCLKFVVSNAENLVD

MADEKPSNGVLVHVMVKLLIKTFLDGI FDDL MENNV LNTDEIHLIGKCLKFVVSNAENLVD
MADEKPSNGVLVHVMVKLLIKTFLDGI FDDL MENNV LNTDEIHLIGKCLKFVVSNAENLVD

hCaspase12

KW-Ap
KW-Bp
KW-Cp
KW-Dp
KW-Ep
KW-Fp
KW-Hp
KW-Gp
KW-Ip
KW-Jp
KW-Kp

DITETAQIAGKIFREHLWNSKKQLSSALLEIQGAQPSGKLKLC PHAHFHELKTKRADEIY
DITETAQIAGKIFREHLWNSKKQLSSDISSDGEREANMPG-----
DITETAQIAGKIFREHLWNSKKQLSSDISSDGEREANMPG-----
DITETAQIAGKIFREHLWNSKKQLSSDISSDGEREANMPG-----
DITETAQIAGKIFREHLWNSKKQLSSDISSDGEREANMPG-----
-----PSGKLKLC PHAHFHELKTKRADEIY
-----AQPSGKLKLC PHAHFHELKTKRADEIY
-----AQPSGKLKLC PHAHFHELKTKRADEIY
-----AQPSGKLKLC PHAHFHELKTKRADEIY
-----AQPSGKLKLC PHAHFHELKTKRADEIY
DITETAQIAGKIFREHLWNSKKQLSSDISSDGEREANMPG-----
DITETAQIAGKIFREHLWNSKKQLSSALLEIQGAQPSGKLKLC PHAHFHELKTKRADEIY

hCaspase12

KW-Ap
KW-Bp
KW-Cp
KW-Dp
KW-Ep
KW-Fp
KW-Hp
KW-Gp
KW-Ip
KW-Jp
KW-Kp

PVMEKERRTCLALNIRNKEFNYLHNRNGSELDLLGMXDLENLGYSVVIKENLTAQEMET
-----LNIRNKEFNYLHNRNGSELDLLGMXDLENLGYSVVIKENLTAQEMET
-----LNIRNKEFNYLHNRNGSELDLLGMXDLENLGYSVVIKENLTAQEMET
-----LNIRNKEFNYLHNRNGSELDLLGMXDLENLGYSVVIKENLTAQ-----
-----LNIRNKEFNYLHNRNGSELDLLGMXDLENLGYSVVIKENLTAQ-----
PVMEKERRTCLALNIRNKEFNYLHNRNGSELDLLGMXDLENLGYSVVIKENLTA-----
PVMEKERRTCLALNIRNKEFNYLHNRNGSELDLLGMXDLENLGYSVVIKESLTAQEMET
PVMEKERRTCLALNIRNKEFNYLHNRNGSELDLLGMXDLENLGYSVVIKENLTAQ-----
PVMEKERRTCLALNIRNKEFNYLHNRNGSELDLLGMXDLENLGYSVVIKENLTAQ-----
PVMEKERRTCLALNIRNKEFNYLHNRNGSELDLLGMXDLENLGYSVVIKENLTAQEMET
-----LNIRNKEFNYLHNRNGSELDLLGMXDLENLGYSVVIKENLTAQEME-
PVMEKERRTCLALNIRNKEFNYLHNRNGSELDLLGMXDLENLGYSVVIKENLTAQEMET

hCaspase12

KW-Ap
KW-Bp
KW-Cp
KW-Dp
KW-Ep
KW-Fp
KW-Hp
KW-Gp
KW-Ip
KW-Jp
KW-Kp

ALRQFAAHPEHQSSDSTFLVFMSHSILNGICGTHWDQEPDVLHDDTIFEIFNNRNCQSL
ALRQFAAHPEHQSSDSTFLVFMSHSILNGICGTHWDQEPDVLHDDTIFEIFNNRNCQSL
ALRQFAAHPEHQSSDSTFLVFMSHSILNGICGTHWDQEPDVLHDDTIFEIFNNRNCQSL

-----SILNGICGTHWDQEPDVLHDDTIFEIFNNRNCQSL
ALRQFAAHPEHQSSDSTFLVFMSHSILNGICGTHWDQEPDVLHDDTIFEIFNNRNCQSL

ALRQFAAHPEHQSSDSTFLVFMSHSILNRI CGTHWDQEPDVLHDDTIFEIFNNRNCQSL
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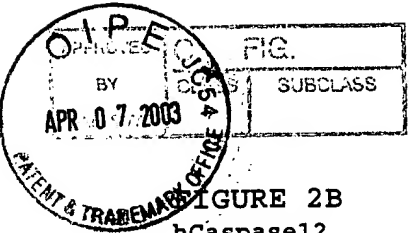


FIGURE 2B

hCaspase12

- KW-Ap
- KW-Bp
- KW-Cp
- KW-Dp
- KW-Ep
- KW-Fp
- KW-Hp
- KW-Gp
- KW-Ip
- KW-Jp
- KW-Kp

KDKPKV IIMQACRGNGAGIVWFTTDSGKASADTHGRLLQGNICNDAVTKAHVEKDFIAFK
KDKPKV IIMQACRGNGAGIVWFTTDSGKASADTHGRLLQGNICNDAVTKAHVEKDFIAFK
KDKPKV IIMQACRGNGAGIVWFTTDSGKASADTHGRLLQGNICNDAVTKAHVEKDFIAFK
-----GAGIVWFTTDSGKASADTHGRLLQGNICNDAVTKAHVEKDFIAFK
-----GAGIVWFTTDSGKASADTHGRLLQGNICNDAVTKAHVEKDFIAFK
KDKPKV IIMQACRG-----
KDKPKV IIMQAC-----
-----GAGIVWFTTDSGKASADTHGRLLQGNICNDAVTKAHVEKDFIAFK
-----MVLGLFGSP
-----MVLGLFGSP
KDKPK-----

KDKPKV IIMQACRGNGAGIVWFTTDSGKASADTHGRLLQGNICNDAVTKAHVEKDFIAFK

hCaspase12

- KW-Ap
- KW-Bp
- KW-Cp
- KW-Dp
- KW-Ep
- KW-Fp
- KW-Hp
- KW-Gp
- KW-Ip
- KW-Jp
- KW-Kp

SSTPHNVSWRHETNGSVFISQIIYYFREYSWSHHLEEIFQKVQHSFETPNILTQLPTIER
SSTPHNVSWRHETNGSVFISQIIYYFREYSWSHHLEEIFQKVQHSFETPNILTQLPTIER
SSTP-----VQHSFETPNILTQLPTIER
SSTPHNVSWRHETNGSVFISQIIYYFREYSWSHHLEEIFQKVQHSFETPNILTQLPTIER
SSTP-----VQHSFETPNILTQLPTIER

SSTPHNVSWRHETNGSVFISQIIYYFREYSWSHHLEEIFQKVQHSFETPNILTQLPTIER
LTVEKPVQILMVGSKVTSVMMLLQRLMWKRTSLLSNLPHHVQHSFETPNILTQLPTIER
LTWKKPVQILMVGSKVTSVMMLLQRFMWKRTSLLSNLPHHVQHSFETPNILTQLPTIER

SSTPHNVSWRHETNGSVFISQIIYYFREYSWSHHLEEIFQKVQHSFETPNILTQLPTIER

hCaspase12

- KW-Ap
- KW-Bp
- KW-Cp
- KW-Dp
- KW-Ep
- KW-Fp
- KW-Hp
- KW-Gp
- KW-Ip
- KW-Jp
- KW-Kp

LSMTRYFYLFPGN
LSMTRYFYLFPGN
LSMTRYFYLFPGN
LSMTRYFYLFPGN

LSMTRYFYLFPGN
LSMTRYFYLFPGN
LSMTRYFYLFPGN

LSMTRYFYLFPGN

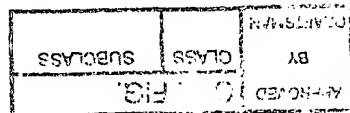


Human Caspase-12 compared to Mouse Caspase-12 with CARD domain, ICE-p20 domain, ICE-p10 domain and Active-site amino acids described.

hCaspase-12	MADEKPSNGVLVHWKLLIKTELDGIFDDLMENNVLNTDEIHLIGKCLKEVVSNAENLV	60
mCaspase-12	MAARRTERDPITYIKGLAKDMLDGVFDDLVKKNVLNGDELLKIGESASFILNKAENLVE	60
hCaspase-12	DITETAQIAGKIFREHLNWSKKLS	85
mCaspase-12	NLEKTDMAKGI FAGHIANSQEQLSQFSDNEDDGPQKICTPSSPSESRRKVEDDEMEVN	120
hCaspase-12	-----SALLEIQGAQPSGKLCLEPHAFHKLTKRADEIYPVMEKERRTCLALN	134
mCaspase-12	AGLAHESHLMLTAPHGLQSSEVQDTLKLCPRDQFCKIKTERAKEIYPVMEKEGRTIALI	180
	↑calpain	
hCaspase-12	IRNKEFNVLHNRNGSELDLGMRDLENIGYSVVIKENLTAQEMETALRQPAHPEHOSS	194
mCaspase-12	ICNKKFDYLFDRNADTDILNQELLENIIGSVVLKENLTAQEMETELMQFAGRPEHOSS	240
hCaspase-12	DSTFLVFMSHGILNGICGTHKWDQEPVLDHDTIFEIENNRNCSLKKPKVIMQACRG	254
mCaspase-12	DSTFLVFMSHGILEGICGVKHRNKKPDVLDHDTIFKIFNNSNCRSLRNKPKILIMQACRG	300
hCaspase-12	NGAGI VWFITDSKASADTHGRLLQGNICNDAYTKAHEKDFIAFKSSTPHNVSWRHETN	314
mCaspase-12	RYNGT IWVSTNKGIAIADTDEERVLSCKWNNSITKAHVEITDFIAFKSSTPHNISWKVGKT	360
	↑auto catalytic	
hCaspase-12	GSVFISQIIYYFREYSWSHLEEIFOKVQHSFETPNILTOLPTIERLSMTRYFYLLFP	373
mCaspase-12	GSLEISKLIDCFKRYCWYHLEEIFRKVQHSFEVPGELTQMPTEIRVSMTRYFYLLFP	419

FIGURE 3

APPROVED	BY	CLASS	SUBCLASS
FIG.			



h_Caspase-3
h_Caspase-7
h_Caspase-12
m_Caspase-12
h_Caspase-4
h_Caspase-13
h_Caspase-5
h_Caspase-1
h_Caspase-6
h_Caspase-8
h_Caspase-10
h_Caspase-9
h_Caspase-2
h_Caspase-14

KPSNGVLVHAKV-----LLIKTFLDGI--FDDIMENNVNTDEIHLICKL-KFVVSNAEN
RTHEROPIYKIK-----GLAKDMLDGV--FDDLVEKNVLNGDELKIGESA-SFILNKAEN
N-HRKPKPLKVL-----SIGKDFLTGV--LDNLVEQNVLNWKEEKKKYD-AKTEDKVRV
K-HNKNPLKMLE-----SIGKELISGL--LDDFVEKNVLKLEEEKKKIYD-AKLQDKARV
N-HKKKTVMLE-----YLGKDV LHGV--FNYLAKHDVLTKEEKKKKYD-AKIEDKALI
KVLKEKRKLFIK-----SMGEGTINGL--LDELQTRVLNKEEMEKVREN-ATVMDKTRA

LFQRLQEKRMLESNLSFLKELLFRINRDLILTYLNTRKEEMERELQTPGRAQISAYRV
VFEEHLLAEDLSEEDPFLLAELLYIIR-QKKLLQHLNCTKEEVERLPTIR-QRVSLFRNN
ADRRLLRRCRLR-----LVEELQVDQMDALLSSELFRPHMIEDIORAGSGSRDQARQ
HPHHQETLKKNR-----VYLAQÖLLSELLEHLLLEKDIITLEMRELIQAKV--GSFSQÑVE

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h_Caspase-3      -----MENTEN-----SVDSK-SIKNLEPKIIH-----GSE-----
h_Caspase-7      -----MADGGCIEEGVEBSANED-----SVDAPDRSSFVPSLFS-----KKKKN-----

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FIGURE 4B

h_Caspase-12
m_Caspase-12
h_Caspase-4
h_Caspase-13
h_Caspase-5
h_Caspase-1
h_Caspase-6
h_Caspase-8
h_Caspase-10
h_Caspase-9
h_Caspase-2
h_Caspase-14

LVDDITETAQIAGKTRFHLMNS-----KKQLSSALL--EIQGAQ----PSG----K---
LVENFLEKTDMAKIFAGHIAN-----QEQLSLQFSNDEDDGPQKICTPSSPSESRRV
MADSMQEKQRMAGQMLQTFENID-----QISPNNKAHPNMEAGPP-----ESGES-----
LVDISIRQKNQEAQVQVQTFENID-----KNSTSIKAPETVAGPD-----ESVGS-----
LVDLSR-KNRVAHQMFQTLNMD-----QKITSVKPLQIEAGPP-----ESAES-----
LIDSVIPKGAQACQICITYICEEDS-----YLAGTIGLSADQTSNGYNLMQDSQGVLSGPPA
-----MSSASGLRGHPAGE-----EN-----
MLYQISEEVSRSLSRFLQIEISKCLDDDMNLDFIEMEKRVILGEGKLDILKRV
LLYELSEGIDSENKDMIFLLKDSLP-KTEMTSLFLAFLEKQK--IDEDNLTCLEDL
LIDLETRGSQALPLFISCLEDTG-----QDMLASFRTNRQAALSKPTLENLTPVVLBP
LNLPLPKRGPAFDFACEALRETQGHLEDMLLTTLGSLQHVLPPLSCDYDLSLFPVCE

h_Caspase-3
h_Caspase-7
h_Caspase-12
m_Caspase-12
h_Caspase-4
h_Caspase-13
h_Caspase-5
h_Caspase-1
h_Caspase-6
h_Caspase-8
h_Caspase-10
h_Caspase-9
h_Caspase-2
h_Caspase-14

-----SMDs--GISLDN-----
-----VTMRS--IKTRDRVPY-----
-----LKICPHAHFHEIKTRADE-----
EDDEMEVNAGLAHES--HLM--LTAPHGLQSEVODTLKCPDQFCIKITERAKE-----
-----TDALKLCPHHEFLRCKERAEE-----
-----AATLKLCPHEEFLRCKERAEE-----
-----TNILKLCPREFLRCKKNHDE-----
PQAVQD-----NPAMPTSSGSEGNVLCSLBEAQRIWKQSAE-----
-----MTETDAFYKREMPDPAE-----
CAQINKSLKIINDY--EFSKERSSSLEGSPEFSGEELCGVMTISDSPREQDSE--
CKTVVPKLLRNIKKYKREKAQIQTVPVDKAEASYGEEELVSQTDVKTFLLEALPQESWQ
EIRK--PEVLRPETPRPYDIGSGFGDVGALLESIRGNAD--
SCPLYKLR-----LSTDVEHSLDNKDGPEVCLQVKPCTPEFYQTHFQ--

h_Caspase-3
h_Caspase-7
h_Caspase-12
m_Caspase-12
h_Caspase-4

-----SYKMDYPEMGLCIIINKN
-----QYNNMFEKLGKCIINKN
-----IYPVMEKERRTCLALNTRN
-----IYPVMEKEGRTLALIICN
-----IYPIKERNNRTRLALIICN

APPROVED	BY	CLASS
0. 59		SUBCLASS



FIGURE 4C

h_Caspase-13
h_Caspase-5
h_Caspase-1
h_Caspase-6
h_Caspase-8
h_Caspase-10
h_Caspase-9
h_Caspase-2
h_Caspase-14

-----IYPIKERDRTIALIICN
-----IYPIKKREDRRRIALLIICN
-----IYPIIMDKSSRTRIALLIICN
-----KYKMDHRRRGIALIFNHER
-----SQTLDKVYQMSKPRGYCLINNHN
NKAHSGNGNRATNGAPSLVSRGMQASANTLNSETSTKRAAVYRMNRNHRGLCVIYNHS
-----LAYILSMPCGHCLINNHN
-----LAYRLQSRPRGLALVSNVH
-----MSNPRSLEBEKYDMGARLLA

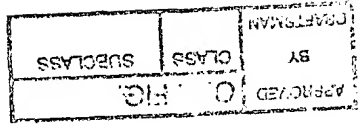
h_Caspase-3
h_Caspase-7
h_Caspase-12
m_Caspase-12
h_Caspase-4
h_Caspase-13
h_Caspase-5
h_Caspase-1
h_Caspase-6
h_Caspase-8
h_Caspase-10
h_Caspase-9
h_Caspase-2
h_Caspase-14

FH-----KSTGMTSRSGTDVDANLRETFRNLKYEVRNK-NDLTREEIVEIMRDVSKE
FD-----KVTGMGVNRNGTDKDAEALFKCFRSLGPDVIVY-NDSCCAKMODLLKASEE
K-----EFNYLHNNGSELDDLGMRLLENLGYSVIKENLTAQEMETALRQFAHP
K-----KFDYLFDRNDADTDILNMQELLENGYSVLKENLTAQEMETELMOTAGR
T-----EFDHLPNRNGADFDITGMKELLEGLDYSDVEENLTARDMESALRAFATRP
T-----EFDHMPNRNGALDILGMKQLLEGLGYTVEVEEKLTAARDMESVLMKFAARE
T-----KFDHLPNRNGAHYDIVGMKRLLOGLGYTVVDEKNLTARDMESVLMKFAARE
E-----EFDSPRRTGAEVDTIGMTMLQNLGYSDVKKNLTAASDMTTELEAFARHP
FF-----WHLTLPERRTCADRDNLTRRFSDLGFEVCKFNDLKAEBLLKIHEVSTVS
FAKAREKVPKLSIRDRNGTHLDAGALLTTTFFELHFEIKPH-DDCTVEQIYEILKIYQLM
F-----TSLKDRQGTBKDAEILSHVFOWLGFVTHNNVTKVEMEMVLOKOKCNP
FCR-----E-SGLRRTGSNIDCEKLRRRFPSSPHFVVEVKGDLTAKKMLALLLELAQOD
FTG-----EKELEFRSGGDVDHSTLVTLFKLLGYDVHVLCDQTAQEMOEKLNFAQLP
L-----ILCVTKAREGSEEDLDALHEMFRQLRFESTMKRDP TAEQFOELEKFOQAI
* * * * *

h_Caspase-3
h_Caspase-7
h_Caspase-12
m_Caspase-12
h_Caspase-4
h_Caspase-13

D--HSKRSSFVCVLLSHGEEG-----IIFGTNG-----PVDLKKITNFFRGDRCSL
D--HTNACFACILLSHGEEN-----VIYKDG-----VTPIKDLTAHFRGDRCKTL
E--HQSDDSTFLVFMH GILN-----GICGTHMDQEPDVLHDDTIFEIFNNRNCQSL
E--HQSDDSTFLVFMHSHGILE-----GICGVKHKRKKPDVLLHDDTIFKI FNNNSNCRSL
E--HKSDDSTFLVLMHSHGILE-----GICGTVHDEKKPDVLLYDTIFQIFNNRNCISL
E--HKSDDSTFLVFMHSHGILD-----GICGTMHSEEPDVL PYDTIFRTFNNRNCISL

APPROVED	BY	CLASS	SUBCLASS
FIG. 4C			



h_caspase-3
h_caspase-7
h_caspase-12
m_caspase-12
h_caspase-4
h_caspase-13
h_caspase-5
h_caspase-1

VDA-DELVAISTARGYYSWRNSKDGSMFIQSLCAMLKQYA-DKLEEMHILTRVNRKVA
VEA-DELEAVSTVPGYYSWRSPGRGSNEVQALCSILEBHG-KDLETMOILTRVNDVRARH
HVEKDFLAFKSTSTPHNVSWRHETNGSVFIQIILYYFREYS-WSHLEIELIQ----KVQHS
HVEITDFIAFKSSTPHNISWKVGKTGSLFISKLIDCFKKYC-WCYHLEIELFR---KVQHS
HVEKDFLAFCSSTPHNVSWRDSTMGSIIFTQILITCFQKYS-WCCHLEEVER---KVQOS
HVEKDFLAFCSSTPHNVSWRDIKKGSLFTRLRLITCFQKYA-WCCHLEEVER---KVQOS
HEEKDFIAFCSSTPHNVSWRDRTRGSIPTTELITCFQKYS-CCCHLEIELFR---KVQKS
HIEKDFLAFCSSTPDNVSWRHPITMGSVFIQRLIEHMQEYA-CSCDVEIELFR---KVRFS



APPROVED	BY	CLASS
0.75		SUBCLASS

FIGURE 4E

h_Caspase-6
h_Caspase-8
h_Caspase-10
h_Caspase-9
h_Caspase-2
h_Caspase-14

PAGADFLMCYSVAEGYSHRETVNGSWYIQDLCEMLGKYG-SSLEFTELLTLVNKVSQR
PDEADFLGMATVNNCVSYRNPAEGTWYIQSLCQSLRERCPRGDDILTILT---EVNVE
PAEADFLGLATVPGYVSFRHVEGWSYIQSLCNHLKJLVPRMLKFEKTM---EIRGR
PTPSDIFVSYSTFPGFVSWRDPKSGSWVETLDDIFEQWA-HSEDLOSL---RVANA
PTSDMICGYACLGTAAMRNTKSGSWIEALAOVSERA-CDMHVADMLVKV-ALIKD
PTYDALHVSTVEGYIAYRHQKSGCFIQTLVDVFTKRK---GHILELLT---EVTRR

h_Caspase-3
h_Caspase-7
h_Caspase-12
m_Caspase-12
h_Caspase-4
h_Caspase-13
h_Caspase-5
h_Caspase-1
h_Caspase-6
h_Caspase-8
h_Caspase-10
h_Caspase-9
h_Caspase-2
h_Caspase-14

FEESFDATEHAKKQIPCIIVSMLTKE--LYFYH---
FESQDDPHFEKKQIPCVVSMILTKE--LYFSQ---
FET----PNILTQPTIERLSMTRYF--YLFPGN---
FEV----PGELTQPTIERVSMTRYF--YLFPGN---
FET----PRAKAQMPPTIERLSMTRYF--YLFPGN---
FEK----PNVKAQMPPTIERLSMTRYF--YLFPGN---
FEV----POAKAQMPPTIERATLTRDF--YLFPGN---
FEQ----PDGRAQMPPTIERATLTRDF--YLFPGH---
RVDFCKDPSAIGKKQVPCFASMLTKK--LHFFPKSN-
VSN--KDDKKNMGKQMPQPTFLRKK--LVFSPD---
KRTWVG-AKQISATSLPTAISAQTPRPPMRWSSVS-
VSV-----KGIYKQMPGCENFLRKK--LFFKTS---
REGYAPGTEFHRCKEMSEYCSLGRH-LYLFPGHPPT
MAEAEVLVQEGKARKTNPEIQSTLKRK--LYLQ-----

- Legend:
- ↓ Active-site Residues
 - * Identical Residues
 - : Conservative Substitution
 - . Allowable Substitution

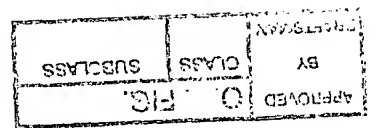
CLUSTAL W (1.7) multiple sequence alignment

FIGURE 5A

```
h_Caspase-4 -----MAEGN-HRKKPLKYLESL
h_Caspase-5 MEKGLQSGLDNFVINHMLKNNVAGQTSIQTLVPNTDQKSTSVKKDN-HKKKTIVKMLEYL
h_Caspase-13 -----MAEDK-HKNPLKMLESL
h_Caspase-12 -----MADEKPSNGVLVHMVKLL
h_Caspase-1 -----MADKVLKEKKKLFIRSM
: . . . .
h_Caspase-4 GKDFLTGVLNDLVEQNVLNWKKEEKKKKYYDAKTEDKVRVMA DSMQEKQRMAGOMLQTEF
h_Caspase-5 GKDV LHGVENYLA KH DVLTLKEEEKKKYYDAKIEDKALILVDSL R-KNRVAHQMFQITLL
h_Caspase-13 GKELISGLDDEVEKNVLKLEEEKKKIYDAKLQDKARVLVDSIRQKNQAGQV FVQITFL
h_Caspase-12 IKTFELDGI FDDLMENNVLNTDEIHLIGKQLK FVVSNAENLVDDITETAQIAGKIFREHLW
h_Caspase-1 GEGTINGLLDELLQTRVLNKEEMEKVKRENATVMDKTRALIDSVIPKGAQACQICITYIC
: *::: : * . . . . : *::: : *::: :
N-----IDQISPNKKAHPNMEAG--PPESGESTDALKLC P
N-----MDQKITSVKPLQIEAG--PPESAESTNLIKLC P
N-----IDKNSTSIKAP EETVAG--PDES VGSATLIKLC P
N-----SKQLSS--ALLEIQA-QP-SGK---LKLCP
EEDSYLAGTLGLSADQTS GNYLNMQDSQGVLSFPAPQAVQDN PAMP TSSGSEGNVKLCS
: . . . . * :***.
h_Caspase-4 HEEFLRLCKERAEEIYPIKERNNRTRLALIICNTEFDHLPRNGADFDITGMKELLEGLD
h_Caspase-5 HEEFLRLCKKNHDEIYPIKKREDRRLALIICNTEKFDHLPARNGAHYDIVGMKRLLQGLG
h_Caspase-13 HEEFLRLCKERAGEIYPIKERKDRTRLALIICNTEFDHMPPRNGALDILGMKQLLEGLG
h_Caspase-12 HAHFHELKTKRADEIYPM EKERRTCLALNIRNKEFNYLHNRNGSELDLLGMRDLLENLG
h_Caspase-1 LEEAQRIMWQKSAEIYPIMDKSSRTRLALIICNEEFDSIPRTGA EVDITGMTMLLQNLG
: . . . . *::: : *::: : *::: : *::: :
h_Caspase-4 YSV DVEENLTAR DMESALRAFA TRPEHKSSDSTFLVLM SHGILEGICGT VHDEKKP DVL
h_Caspase-5 YTVVDEKNLTAR DMESVLRAFA RPEHKSSDSTFLVLM SHGILEGICGT AHKKKPDVLL
h_Caspase-13 YTVEVEEKL TAR DMESVLWKFA REEHKSSDSTFLVMS HGILD GICGTMHSEEPDVL P
h_Caspase-12 YSVVIKENLT AQEMETALRQFAA HPEHQSSDSTFLVMS HGILNGICG TKHWDQEPDVLH
```

APPROVED	BY	CLASS	SUBCLASS





h_Caspase-1

```
Y$VDVKKNL$TASDMITTELEAF$HPRPEHKTS$D$TFLVFM$HGIRREGICGK$H$SE$OVPDILQ
*:*::*:;*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*
```

```
YDTIFQIENNRRNCLSLDKPKVIIIVQACRGANGELMVR-DSPASLEVAASSQSE-NLEE  
YDTIFEIENNRNCLSLDKPKVIIIVQACRGEKHEGLMVR-DSPASLAVISSQSE-NLEA  
YDTIFERTENRNCLSLDKPKVIIIVQACRGANGELMVS-DSPALADSSQSE-NLEE  
DPTIEEIEFNRRNCQSLDKPKVIIIMQACRGNGAGI-VWFTTDSKASADTHGRLLQGNCN  
LNALFNMNLNTKNCPSLDKPKVIIIVQACRGDSPGVWF-K-DSVGSGNLSPTTE-EFED  
::*:.*:*****:*:*:**
```

DAVYKTHVEKDFIAFCSSTPHNVSWRDSTMGSLFITQLITCFOKYMSWCCHLBEVERKVOQ
 DAVYKTHVEKDFIAFCSSTPHNVSWRDRTGRGSLFITBELITCFOKYSCCCHLMEIFRKVOK
 DSVCKIHEEKDFIAFCSSTPHNVSWRDITRGSLFITBELITCFOKYSCCCHLMEIFRKVOK
 DAVYKTHVEKDFIAFCSSTPHNVSWRDITKKGSLFITRLITCFOKYAMCCHLBEIFRKVOQ
 DAVYKTHVEKDFIAFCSSTPHNVSWRHETNGSVFISQIIYYFEREYSWCHLBEIEFOKVQ
 DAIKKAHIEKDFIAFCSSTPDNVSWRHPMTGWSVFIGRLIEHMOEYACSCVBEIEIFRKVRF
 : : : * * * * * : : : : : * * * * * : : : : : * * * * * : : : : : * * * * *

```

SFEETPRAKAQMPTEIRLSMTRYFYLLFPNG
SFEVPOAKAQMPTEIRATLTRDFYLLFPNG
SFEKPNUVAKQMPTEIRLSMTRYFYLLFPNG
SFEETPNILLQPLTEIRLSMTRYFYLLFPNG
SFEQDPGRAQMPTEIRVTLTRCFYLLFPNG
*** * : * * * * : * * * * :

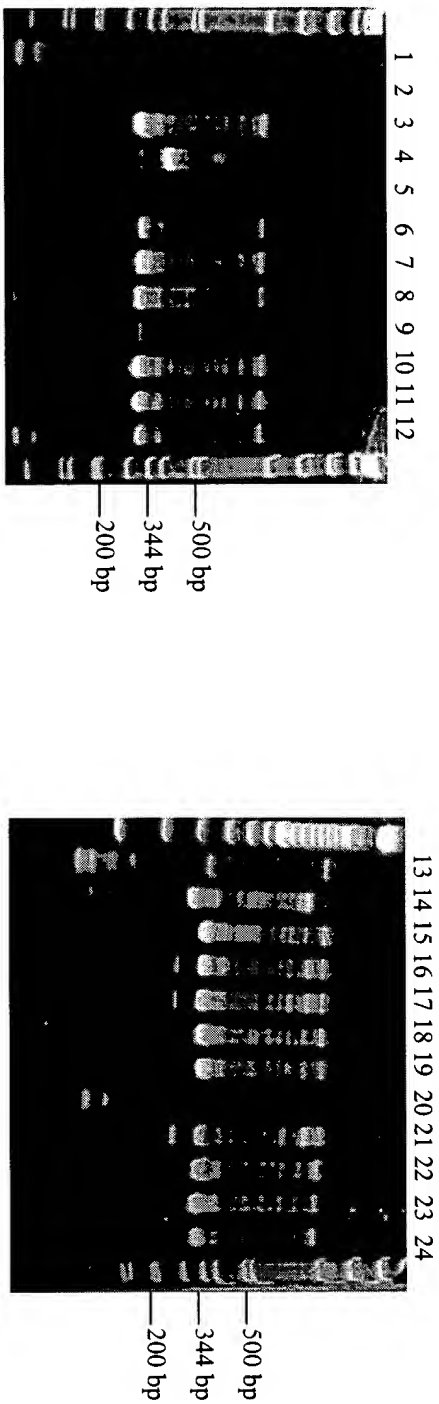
```

Active-site Residues

APPROVED	O. FIG.	CLASS	SUBCLASS
BY			
DATE			



FIGURE 6



1. Brain 2. Heart 3. Kidney 4. Spleen 5. Liver 6. Colon 7. Lung 8. Small Intestine
9. Muscle 10. Stomach 11. Testis 12. Placenta 13. Pituitary 14. Thyroid gland
15. Adrenal gland 16. Pancreas 17. Ovary 18. Uterus 19. Prostate 20. PBL 21. Fetal brain
22. Fetal liver 23. Fat 24. Mammary gland

APPROVED	BY	CLASS	SUBCLASS

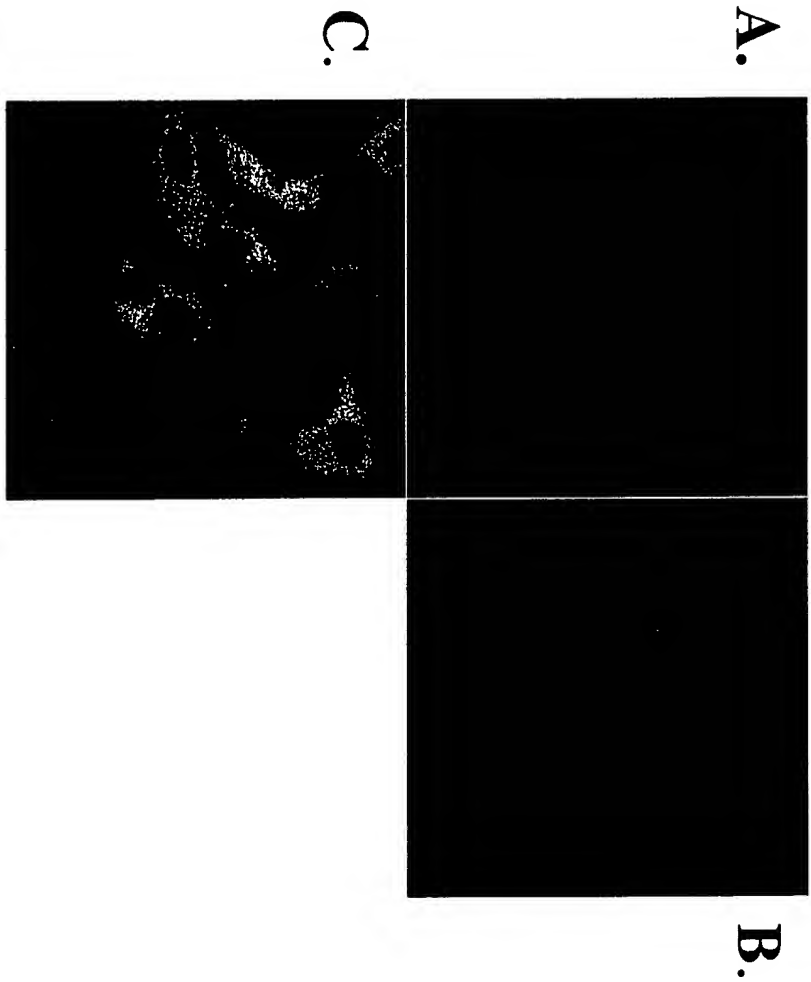
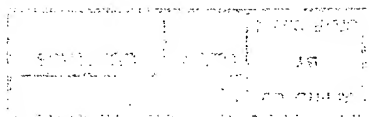
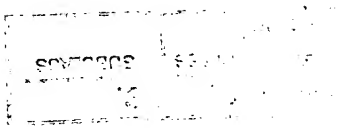


FIGURE 7





A.

Procaspase-3 →

p19 cleavage product

No lysate

hCaspase-12

Δ CARD

control

W.

Caspase-3 Active

→ p19

hCaspase-12

No lysate

ΔCARD

FIGURE 8



FIGURE 9

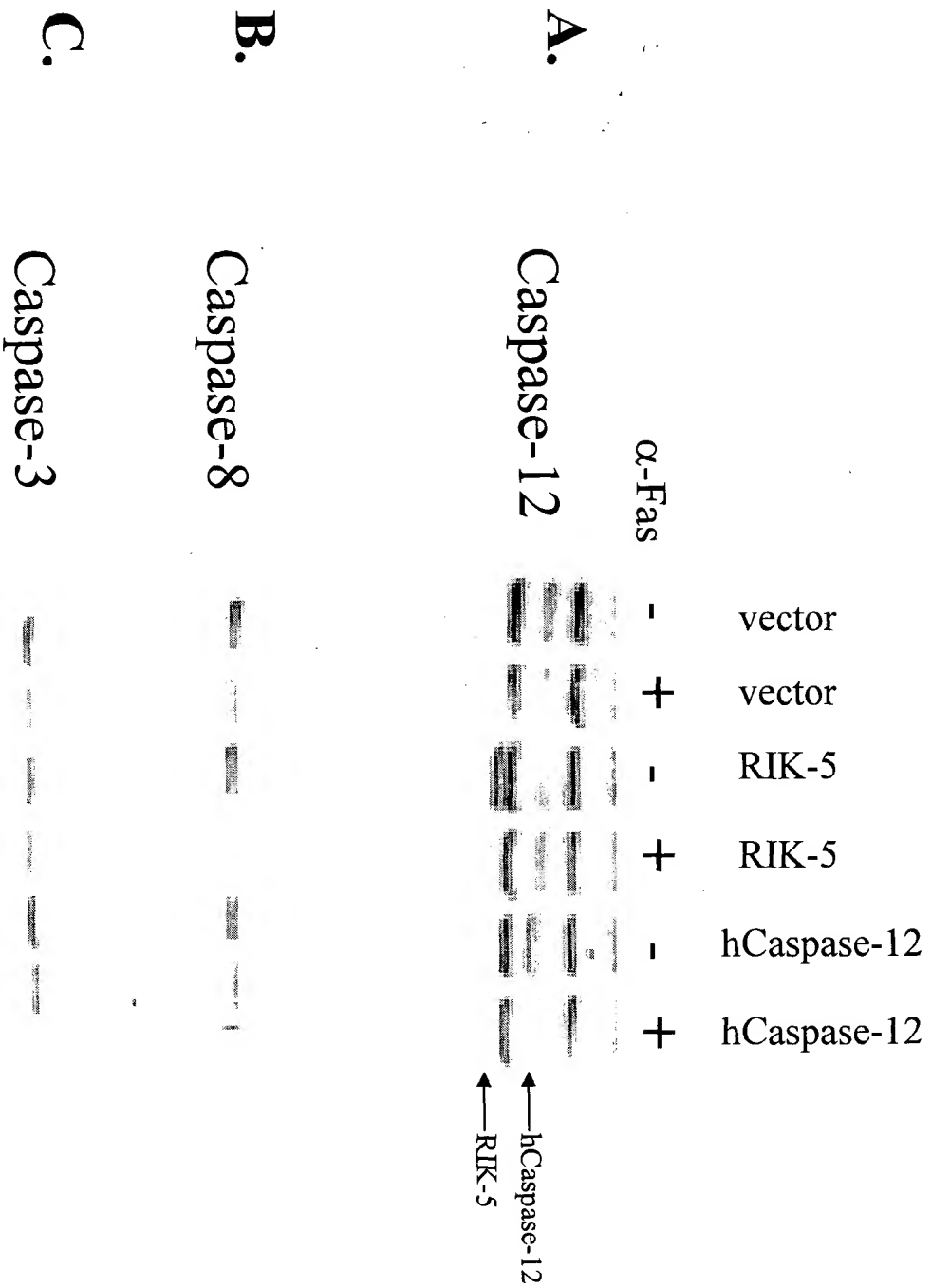
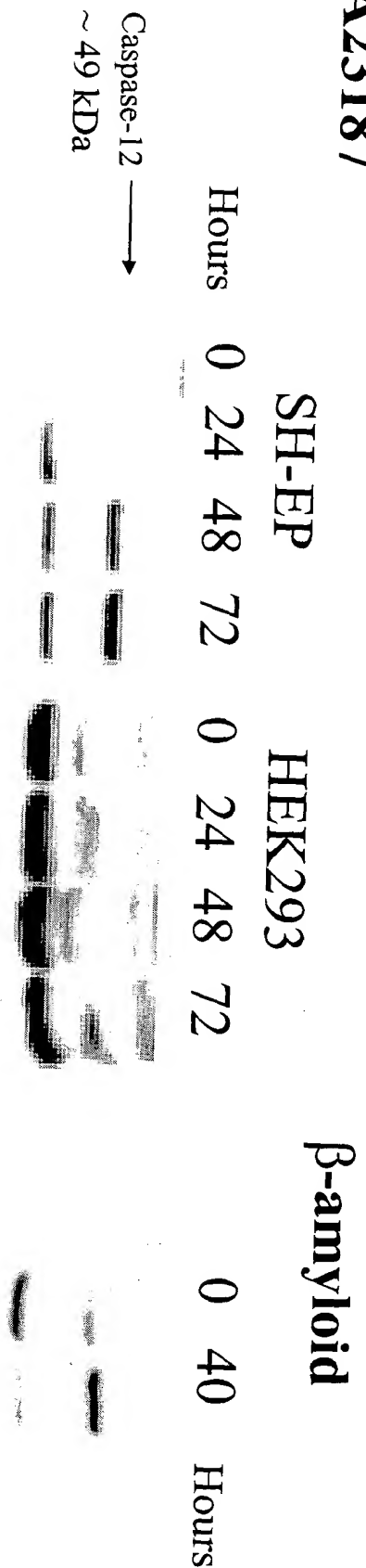


FIGURE 10

A23187



Tunicamycin

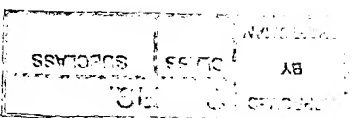
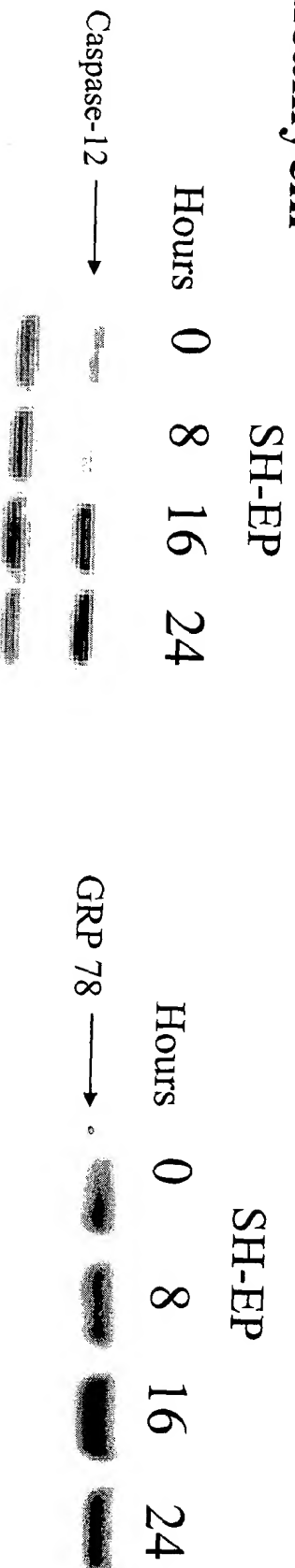




FIGURE 11

A.

Caspase-12 →

Untreated

A23187

A23187, CHX

A23187, UV

A23187, α -Fas

B.

Caspase-3 →

C.

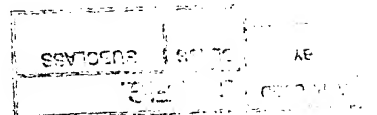


FIGURE 12

A.

- 1.
- 2.
- 3.
- 4.

Caspase-12



B.

Caspase-3

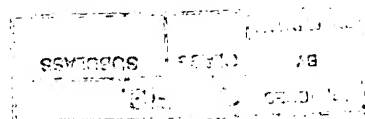
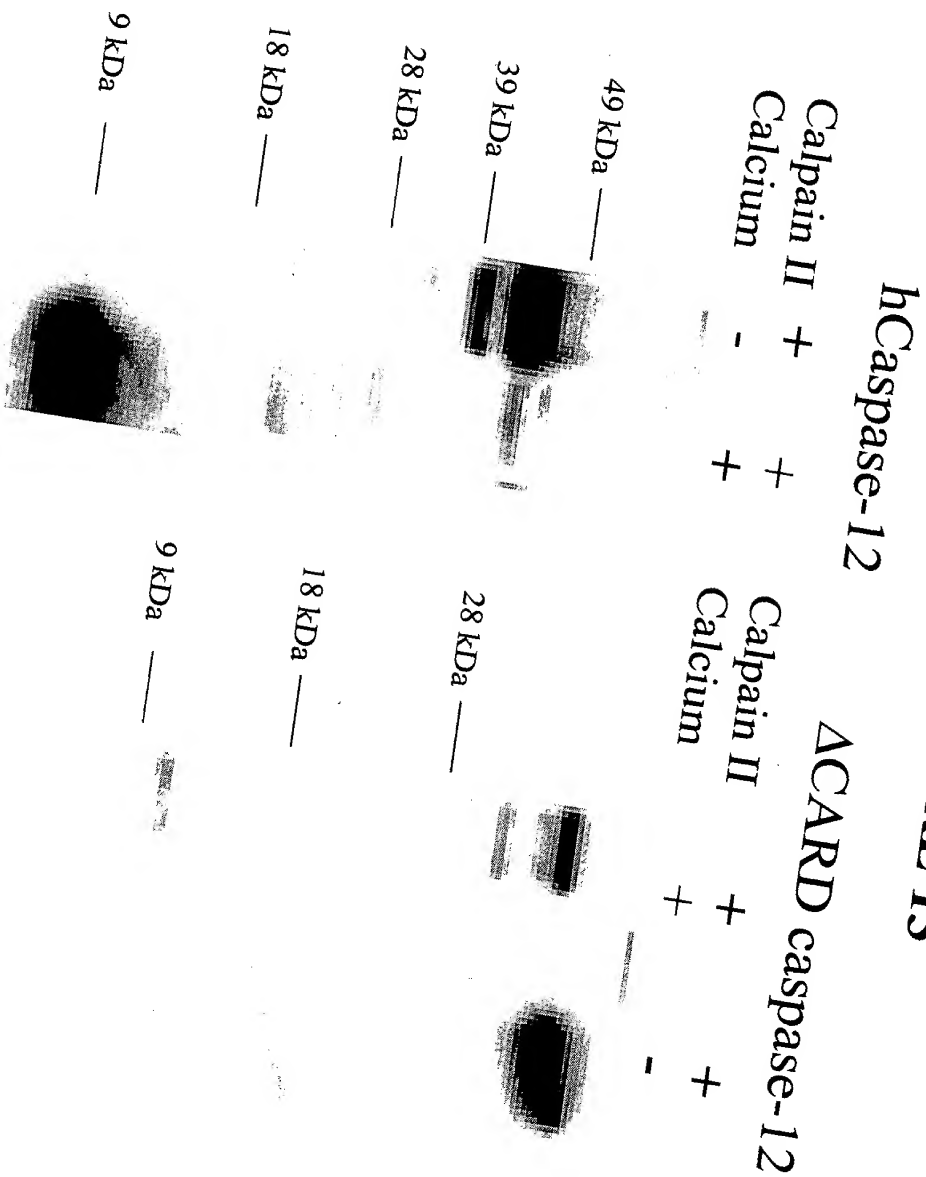




FIGURE 13



Subcellular
Fractionation